

G. Leffers

**ENTERED**

1636

#9  
S.Q.  
8/24/00

RAW SEQUENCE LISTING DATE: 08/15/2000  
PATENT APPLICATION: US/09/430,590A TIME: 11:58:10

DATE: 08/15/2000

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Input Set : A:\ES.txt  
Output Set: N:\CRF3\08152000\I430590A.raw

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AUG 22 2003

TECH CENTER 1600/2000

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106 gggtttggaa tggatcaca ctatcaaaaag agtattggaa gacattgggtt ttactcaagt 5040  
 107 ttatatatgtt gatgatattc ttatgggtgg aagttcacaa aaagtttattg ataattttgt 5100  
 108 ggataatttg agagatcatt tgaaagttaa agtgtttgggt gaaatataaa attatcttgg 5160  
 109 tatttataattt cgtaaaaaaccg aatctgggtt tattttatct caagaaaaaa ttctcaagaa 5220  
 110 attacttaag gatttcaaacc tagatgactc atatgggaaa aacataccct ggattccgaa 5280  
 111 tgacaaaatat gaaaagggtt caataattcg tgaaaacgtt aatccagaga atgattttga 5340  
 112 aaagggttcg aatgagacat tgcttgacc tgatgctaa aaactatacc aaagtgggtt 5400  
 113 tggctgtctt ttatgggtcg cccaaacac acgtcccatg atatcggtcg tagtgaattc 5460  
 114 gttgggttctt aatctgcac accaaatgtt ccattgattt gagaatgtt tttattgtt 5520  
 115 taggtatatac aaaaatagca tgggatatac cattgagttt aaaaagaaaca gattgaat 5580  
 116 accaccaaaa tcatttggta tgcattttttt cagtttttttgcac caggatttggaa 5640  
 117 tagaaaaatctt attatggaa ctttgattt tgcatttttttgc aatggggcacc 5700  
 118 caaaaaaaaa acggccatag cccaaatgtt acgtcccatg atatcggtcg tagtgaattt 5760  
 119 tacaatgttgg aagctatcg aataaaaaaa ccattttatgtt gattttgggtt ttgaagttt 5820  
 120 taagatatacat tgcattcaag acaaccaacg tgcatttttttgc aatactattt 5880  
 121 tcacccacat cgaccaatag atatcggttttgc tgcatttttttgc tcaatgataa 5940  
 122 agtattttca atatcttgc tgcatttttttgc tgcatttttttgc tgcatttttttgc 6000  
 123 tctaatttttttgc tgcatttttttgc tgcatttttttgc tgcatttttttgc tgcatttttttgc 6060  
 124 agataatcaa acactgatac aaaaatgtt aacggccatg tgcatttttttgc tgcatttttttgc 6120  
 125 attatcgtaatc tgcattcaatc ggggatgtttt gtttttttttttgc tgcatttttttgc tgcatttttttgc 6180  
 126 atcaatgttgg atatgttttttgc tgcatttttttgc tgcatttttttgc tgcatttttttgc 6240  
 127 gacagaacta aactatatttgc tgcatttttttgc tgcatttttttgc tgcatttttttgc tgcatttttttgc 6300  
 128 tatcaacggatagaaggaa gggatgttttttgc tgcatttttttgc tgcatttttttgc tgcatttttttgc 6360  
 129 aatttcaatc acacaactatcg acgtgttgc tgcatttttttgc tgcatttttttgc tgcatttttttgc 6420  
 130 cccatca 6426  
 133 <210> SEQ ID NO: 2  
 134 <211> LENGTH: 324  
 135 <212> TYPE: PRT  
 136 <213> ORGANISM: Candida albicans  
 138 <400> SEQUENCE: 2  
 139 Met Ser Ser Ala Lys Asn Asp Asp Asn Glu Gly Lys Val Met Glu Ser  
 140 1 5 10 15  
 142 Val Asp Gln Ala Asn Ala Ile Ser Lys Val Asp Glu His Ile Lys Ala  
 143 20 25 30  
 145 Arg Phe Asn Met Leu Phe Ile Lys Phe Asn Asp Leu Pro Lys Leu Ala  
 146 35 40 45  
 148 Val Gly Asn Gln Lys Ser Val Asp Lys Trp Asn Glu Glu Phe Lys Tyr  
 149 50 55 60  
 151 Phe His Val Ala Tyr Pro Asp Val Leu Glu Phe Leu Leu Asp Tyr Asn  
 152 65 70 75 80  
 154 Pro Lys Asp Lys Phe Lys Val Lys Val Glu Gly Ile Tyr Phe Thr  
 155 85 90 95  
 157 Gly Trp Cys Leu Gln Met Cys Leu Gln Ser Ile Phe Asp Arg Phe Arg  
 158 100 105 110  
 160 Leu Ile Met Ile Ser Lys Leu Pro Lys His Leu Gln Lys Glu Ala Asn  
 161 115 120 125  
 163 Leu Ile Lys Ala Ala Tyr Asp Ala Val Thr Lys Ser Lys Asp Tyr Thr  
 164 130 135 140  
 166 Ile Thr Ser Lys Ile Leu Ser Lys Phe Val Asn Val Glu His Glu Leu

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167 145      150      155      160
169 Val Val Cys Tyr Asn Leu Pro Tyr Leu Ser Gln Val Glu Glu Lys Leu
170          165      170      175
172 Glu Glu Ile Leu Tyr Asn Thr Ser Asn Val Val Asp Glu Tyr Val Arg
173          180      185      190
175 Ser Leu Pro Asn Leu Ile Gly Gln Val Leu Tyr Phe Asn His Val Lys
176          195      200      205
178 Lys Ser Glu Ala Leu Ser Leu Phe Leu Asn Ile His Ala Ser Tyr Tyr
179          210      215      220
181 Ser Lys Trp Ile Gln Ala Asp Asn Asp Thr Ser Val Leu Pro Ser Cys
182 225      230      235      240
184 Ser Thr Ile Ala Glu Glu Met Cys Asp His Pro Asp Tyr Ala Arg Leu
185          245      250      255
187 Val Asp Ile Pro Ser Asn Lys Tyr Glu Leu Asn Leu Ile Val Ser Leu
188          260      265      270
190 Pro Ala Pro Glu Lys Pro Lys Gly Lys Pro Glu Glu Asn Ser Ser Glu
191          275      280      285
193 Gln Ser Gln Lys Lys Asn Ser Lys Ser Arg Lys Arg Asn Lys Lys His
194          290      295      300
196 Pro Lys Ser Asp Asn Asp Lys Gly Glu Lys Glu Lys Glu Lys Glu Lys
197 305      310      315      320
199 Thr Ser Ser Glu
203 <210> SEQ ID NO: 3
204 <211> LENGTH: 1576
205 <212> TYPE: PRT
206 <213> ORGANISM: Candida albicans
208 <400> SEQUENCE: 3
209 Lys Thr Gly Ala Ala Ser Ile Asn Cys Val Met Asn Ile His Asn Cys
210 1          5          10         15
212 Ser Lys Thr Thr Phe Pro Val Glu Asn Ser His Ser Leu Asn Ala Ser
213          20          25         30
215 Leu Asn Val Met Asn Phe Lys Gly Leu Arg Phe Asn Lys Tyr Leu Val
216          35          40         45
218 Tyr Asp Thr Gly Ala Thr Ile Ser Val Val Asn Asn Lys Asp Ile Leu
219          50          55         60
221 Ser Asn Val Lys Asp Ala Thr Ile Glu Val Ser Val Ala Asp Gly Ala
222          65          70         75         80
224 Thr Leu Glu Ala Asp Cys Ile Gly Asp Leu Ile Ile Arg Val Gly Ile
225          85          90         95
227 Val Ser Ile Thr Leu Glu Asn Thr Leu Tyr Leu Pro Glu Ser Ser Phe
228          100         105        110
230 Asn Leu Val Ser Leu Lys Gln Ile Glu Glu Arg Gly Phe Asn Val Leu
231          115         120        125
233 Ile Thr Lys Glu Ser Val Ile Val Phe Asn Gln Asn Val Ala Pro Thr
234          130         135        140
236 Ile Ile Ala Ser Arg Lys Asn Ala Ala Asp Leu Tyr Met Gly Pro Gln
237 145      150      155      160
239 Phe Ser Glu Glu Ser Leu Glu Cys Asp Phe Asp Tyr Asp Gly Leu Ala
240          165         170        175

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```

242 Asp Met Leu Ser Asn Ala Asn Gln Asp Asp Lys Asp Lys Ser Ser Met
243           180          185          190
245 Asn Glu Met Ser Glu Tyr Gln Glu His Asp Tyr Ser Ser Arg Ala Leu
246           195          200          205
248 Ile Asn Ser Leu Thr Glu Val Asp Val Leu Asp Val Glu Ile Ser Pro
249           210          215          220
251 Tyr Gly Val Glu Gln Leu Leu Pro Thr Gly Asp Lys Asn Asp Ile Tyr
252           225          230          235          240
254 Asn Phe His Leu Met Ser Asn His Met Ser Ile Glu Lys Ile Leu Leu
255           245          250          255
257 Leu Gln Lys Tyr Gln Gly Leu Val Leu His Thr Ser Lys Glu Ser Leu
258           260          265          270
260 Gln Lys Ile Ala Asp Cys Lys Val Cys Leu Leu Ser Asn Ala Lys Gln
261           275          280          285
263 Arg Ser His Asn His His Ser Glu Arg Lys Ala Ser Arg Arg His Glu
264           290          295          300
266 Arg Leu His Cys Asp Thr Leu Gly Pro Phe Arg Ser Glu Asn Asn Lys
267           305          310          315          320
269 Trp Tyr Leu Thr Ser Val Ile Asp Glu His Thr Gly Tyr Ile Glu Gly
270           325          330          335
272 Ile Ile Thr Lys Asp Arg Lys Val Lys Asp Leu Leu Ile Gln Arg Leu
273           340          345          350
275 Lys Ile Trp Asn Asn Arg Phe Asn Asp Lys Val Ala Tyr Phe Arg Ser
276           355          360          365
278 Asp Asn Ala Pro Glu Phe Pro Gln Pro Ser Asp Leu Ala Glu Phe Gly
279           370          375          380
281 Ile Trp Arg Glu Thr Ile Ala Ala Tyr Ser Pro Glu Leu Asn Gly Leu
282           385          390          395          400
284 Ala Glu Val Val Asn Lys Leu Ile Leu Gln Gln Ile Tyr Arg Ile Val
285           405          410          415
287 Val Thr Leu Gly Pro Gln Ile Leu Lys Leu Ile Tyr Tyr Val Ile Gln
288           420          425          430
290 Tyr Ser Ile Thr Met Ile Asn His Thr Pro Arg Arg Ser Leu Lys Gly
291           435          440          445
293 Gln Thr Pro Tyr Gly Cys Tyr Tyr Gln Leu Ser Glu Gly Asn Phe Tyr
294           450          455          460
296 Arg Phe Pro Phe Ala Ile Asp Cys Val Val Thr Phe Ser Asn Ala Ile
297           465          470          475          480
299 Glu Lys Asn Arg Tyr Gly Val Thr Ser Thr Lys Gly Ala Pro Ser Ser
300           485          490          495
302 Ile Met Gly Ala Val Ile Gly Tyr Ala Ser Asp Cys Phe Ser Tyr Tyr
303           500          505          510
305 Val Leu Leu Lys Asn Met Arg Cys Asp Ile Ile Leu Ser Pro Asn Val
306           515          520          525
308 Arg Ile Leu Arg Ser Tyr Glu Val Ile Asn Ser Tyr Leu Lys Asn Leu
309           530          535          540
311 Ser Thr Thr Pro Met Ser His Ile Val Pro Met Ala Glu Gly Ile Gln
312           545          550          555          560
314 Gly Arg Gln Ser Gly Ala Gln Tyr Glu Val Arg Gly Thr Tyr Val Glu

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